Query= SEQ ID NO:9 (PE029)
          (184 letters)

                                                           Score   E
Sequences producing significant alignments: (bits)   Value

AL390242.17.1.68883   192   5e-47
AL158844.14.1.53402   78   8e-13

>AL390242.17.1.68883
          Length = 68883

 Score = 192 bits (97), Expect = 5e-47
 Identities = 97/97 (100%)
 Strand = Plus / Plus

Query: 88   agcacaccaacatggcacatgtatacatatgtaacaaacctgcacattgtgcacatgtac 147
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3247 agcacaccaacatggcacatgtatacatatgtaacaaacctgcacattgtgcacatgtac 3306

Query: 148   cctaaaacttaaagtgtaacaataataaaattttttt 184
             |||||||||||||||||||||||||||||||||||||
Sbjct: 3307 cctaaaacttaaagtgtaacaataataaaattttttt 3343

>AL158844.14.1.53402
          Length = 53402

 Score = 77.8 bits (39), Expect = 8e-13
 Identities = 45/48 (93%)
 Strand = Plus / Plus

Query: 40   actgntgtttgcaagctgnntaagtgagcaaatcttgggaagatttca 87
             |||| ||||||||||||| ||||||||||||||||||||||||||||
Sbjct: 53105 actgttgtttgcaagctggttaagtgagcaaatcttgggaagatttca 53152

Query= SEQ ID NO:10 (PE029)
          (309 letters)

	Score (bits)	E Value
Sequences producing significant alignments:		
AC087564 ACCESSION:AC087564 NID: gi 28933558 gb AC087564.6 Hom...	589	e-165
AC007344 ACCESSION:AC007344 NID: gi 5851724 gb AC007344.3 AC007...	589	e-165

>AC087564 ACCESSION:AC087564 NID: gi 28933558 gb AC087564.6 Homo sapiens
            chromosome 16 clone RP11-437L7, complete sequence
          Length = 157233

 Score = 589 bits (297), Expect = e-165
 Identities = 309/310 (99%), Gaps = 1/310 (0%)
 Strand = Plus / Minus

Query: 1   ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 105042 ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 104983

Query: 61   gtgacatggagggtcccccacctgcaagcttttgtgtttgctggatcttggacagtacc 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 104982 gtgacatggagggtcccccacctgcaagcttttgtgtttgctggatcttggacagtacc 104923

Query: 121   ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatatct 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 104922 ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatatct 104863

Query: 181   aacaccttgttccct-ttgcggttcaaaagccactgtcactggggtacataggcagtttt 239
               ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 104862 aacaccttgttcccttttgcggttcaaaagccactgtcactggggtacataggcagtttt 104803

Query: 240   aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 299
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 104802 aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 104743

Query: 300   gttgaaacgc 309
               ||||||||||
Sbjct: 104742 gttgaaacgc 104733

>AC007344 ACCESSION:AC007344 NID: gi 5851724 gb AC007344.3 AC007344 Homo
          sapiens chromosome 16 clone RPCI-11_466G2, complete
          sequence
       Length = 180827

 Score = 589 bits (297), Expect = e-165
 Identities = 309/310 (99%), Gaps = 1/310 (0%)
 Strand = Plus / Plus

Query: 1   ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 176532   ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 176591

Query: 61   gtgacatggagggtcccccacctgcaagcttttgtgtttgctggatcttggacagtacc 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 176592   gtgacatggagggtcccccacctgcaagcttttgtgtttgctggatcttggacagtacc 176651

Query: 121   ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatatct 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 176652   ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatatct 176711

Query: 181   aacaccttgttccc-tttgcggttcaaaagccactgtcactggggtacataggcagtttt 239
                ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 176712   aacaccttgttcccttttgcggttcaaaagccactgtcactggggtacataggcagtttt 176771

Query: 240   aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 299
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 176772   aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 176831

Query: 300   gttgaaacgc 309
                ||||||||||
Sbjct: 176832   gttgaaacgc 176841

Query= SEQ ID NO:11 (PE029)
          (143 letters)

```
                                                            Score      E
Sequences producing significant alignments:                (bits)   Value

AC019129 ACCESSION:AC019129 NID: gi 16077059 gb AC019129.8  Hom...     266   1e-68


>AC019129 ACCESSION:AC019129 NID: gi 16077059 gb AC019129.8   Homo
            sapiens BAC clone RP11-559M23 from 2, complete sequence
          Length = 172611

 Score =  266 bits (134), Expect = 1e-68
 Identities = 140/143 (97%)
 Strand = Plus / Minus


Query: 1       gtggccatgtacttggcttaaagttaaggattctactactgtngaaganggagagaacgg 60
               |||||||||||||||||||||||||||||||||||||||||||| ||||! |||||||||||
Sbjct: 94486   gtggccatgtacttggcttaaagttaaggattctactactgtagaagaaggagagaacgg 94427


Query: 61      nttctagaggacaactggcagtctccttgtagctgagactttttgtgtataaaaattaa 120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 94426   attctagaggacaactggcagtctccttgtagctgagactttttgtgtataaaaattaa 94367


Query: 121     taaaattggtttattaatttgtt 143
               |||||||||||||||||||||||
Sbjct: 94366   taaaattggtttattaatttgtt 94344
```

Query= SEQ ID NO:12 (PE029)
     (210 letters)

```
                                                               Score      E
Sequences producing significant alignments:                   (bits)   Value

AC016601.7.1.145264                                             281     8e-74
AC034246.4.1.155025                                             281     8e-74
```

>AC016601.7.1.145264
        Length = 145264

 Score = 281 bits (142), Expect = 8e-74
 Identities = 146/147 (99%), Gaps = 1/147 (0%)
 Strand = Plus / Minus

```
Query: 64     agagatgggggtttcgccatgttgcccaggctggtctcaagctcctgaactcaagtgatc 123
              ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36474  agagat-ggggtttcgccatgttgcccaggctggtctcaagctcctgaactcaagtgatc 36416


Query: 124    ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36415  ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 36356


Query: 184    aaatatagattttaatcttcagcttgc 210
              |||||||||||||||||||||||||||
Sbjct: 36355  aaatatagattttaatcttcagcttgc 36329
```


 Score = 129 bits (65), Expect = 7e-28
 Identities = 65/65 (100%)
 Strand = Plus / Minus

```
Query: 1      atctatgcagattagctctctgcccttcctttaataactggactcttggagcatctgatt 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 43711  atctatgcagattagctctctgcccttcctttaataactggactcttggagcatctgatt 43652


Query: 61     gacag 65
              |||||
Sbjct: 43651  gacag 43647
```

>AC034246.4.1.155025
          Length = 155025

 Score = 281 bits (142), Expect = 8e-74
 Identities = 146/147 (99%), Gaps = 1/147 (0%)
 Strand = Plus / Plus

Query: 64   agagatgggggtttcgccatgttgcccaggctggtctcaagctcctgaactcaagtgatc 123
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16092 agagat-ggggtttcgccatgttgcccaggctggtctcaagctcctgaactcaagtgatc 16150

Query: 124   ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 16151 ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 16210

Query: 184   aaatatagattttaatcttcagcttgc 210
              |||||||||||||||||||||||||||
Sbjct: 16211 aaatatagattttaatcttcagcttgc 16237

 Score = 129 bits (65), Expect = 7e-28
 Identities = 65/65 (100%)
 Strand = Plus / Plus

Query: 1   atctatgcagattagctctctgcccttcctttaataactggactcttggagcatctgatt 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8857   atctatgcagattagctctctgcccttcctttaataactggactcttggagcatctgatt 8916

Query: 61   gacag 65
              |||||
Sbjct: 8917   gacag 8921

Query= SEQ ID NO:13 (PE029)
          (453 letters)

	Score	E
Sequences producing significant alignments:	(bits)	Value

AL391500 ACCESSION:AL391500 NID: gi 12227422 emb AL391500.13 H...   735   0.0

>AL391500 ACCESSION:AL391500 NID: gi 12227422 emb AL391500.13 Human DNA
          sequence from clone RP11-707M13 on chromosome 6, complete
          sequence
          Length = 171220

 Score = 735 bits (371), Expect = 0.0
 Identities = 371/371 (100%)
 Strand = Plus / Minus

Query: 1   gtatacatccagatggccggaagcaactgaagatccacaaaagaagtgaaaatagccgta 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 76957 gtatacatccagatggccggaagcaactgaagatccacaaaagaagtgaaaatagccgta 76898

Query: 61   actgatgacattccaccattgtgatttgtttctgccccaccgtaactgatcaatgtactt 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 76897 actgatgacattccaccattgtgatttgtttctgccccaccgtaactgatcaatgtactt 76838

Query: 121   tgtaatctcccccacccttaagaaggttctttgtaatctcccccacccttaagaatgttc 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 76837 tgtaatctcccccacccttaagaaggttctttgtaatctcccccacccttaagaatgttc 76778

Query: 181   tttgtaattctcccccacccttgagaatgtactttgtgagatctacccccctgcccacaaaa 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 76777 tttgtaattctccccacccttgagaatgtactttgtgagatctaccccctgcccacaaaa 76718

Query: 241   cattggtcctgactccaccgcctatcccaaaacctataagaactaatgataatcccacca 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 76717 cattggtcctgactccaccgcctatcccaaaacctataagaactaatgataatcccacca 76658

Query: 301   ccctttgctgactctcttttcggactcagcccgcctgcacccaggtgaaataaacagcct 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 76657 ccctttgctgactctcttttcggactcagcccgcctgcacccaggtgaaataaacagcct 76598

Query: 361   tgttgctcaca 371
              |||||||||||
Sbjct: 76597 tgttgctcaca 76587

```
                                                                    Score      E
Sequences producing significant alignments:                        (bits)   Value

AL354814.19.1.70126                                                  281     1e-73
AL391683.8.1.168373                                                  238     2e-60
AL160397.17.1.204056                                                 163     2e-38


>AL354814.19.1.70126
         Length = 70126

 Score =  281 bits (142), Expect = 1e-73
 Identities = 145/146 (99%)
 Strand = Plus / Plus


Query: 199   caggaagaaaaatggaactaaaaagggaaaacaatagcaacaaagatcaaaataaataac 258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 25129 caggaagaaaaatggaactaaaaagggaaaacaatagcaacaaagatcaaaataaataac 25188


Query: 259   aaggaagcggagagaagaaagaacatggtgaagagagtgaaaagcattgtcatttggggt 318
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 25189 aaggaagcggagagaagaaagaacatggtgaagagagtgaaacgcattgtcatttggggt 25248


Query: 319   gaattgcagaaagaaataaattattg 344
             ||||||||||||||||||||||||||
Sbjct: 25249 gaattgcagaaagaaataaattattg 25274



>AL391683.8.1.168373
         Length = 168373

 Score =  238 bits (120), Expect = 2e-60
 Identities = 120/120 (100%)
 Strand = Plus / Plus


Query: 83     aatttcgctcttgttgcccaggctggagtgcaatgacgagatcttggctcactgcaacct 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140792 aatttcgctcttgttgcccaggctggagtgcaatgacgagatcttggctcactgcaacct 140851


Query: 143    ccacctcccaggtttaagtgattctcctgcctcagcctcccaagtagctgggattacagg 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 140852 ccacctcccaggtttaagtgattctcctgcctcagcctcccaagtagctgggattacagg 140911
```

>AL160397.17.1.204056
        Length = 204056

 Score = 163 bits (82), Expect = 2e-38
 Identities = 82/82 (100%)
 Strand = Plus / Plus

Query: 1   tgcctccagaaagaacgcagccctactgacaccttggtttttggcctggtgagaccaactt 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1502 tgcctccagaaagaacgcagccctactgacaccttggtttttggcctggtgagaccaactt 1561

Query: 61   tggactttttcacttccaaaact 82
             ||||||||||||||||||||||
Sbjct: 1562 tggactttttcacttccaaaact 1583

Query= SEQ ID NO:15 (PE029)
         (473 letters)

```
                                                                Score      E
Sequences producing significant alignments:                    (bits)   Value

AC084117 ACCESSION:AC084117 NID: gi 22165345 gb AC084117.6  Hom...   414   e-113


>AC084117 ACCESSION:AC084117 NID: gi 22165345 gb AC084117.6   Homo
         sapiens chromosome 11, clone RP11-107C21, complete
         sequence
         Length = 166973

 Score =  414 bits (209), Expect = e-113
 Identities = 215/217 (99%)
 Strand = Plus / Minus


Query: 192    caggtctacatttctctttgccatactgctctgggctctggggggttgacctgaatggacc 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84399  caggtctacatttctctttgccatactgctctgggctctggggggttgacctgaatggacc 84340


Query: 252    acacagccatggtgtctcctgtcctccaccttcactggtgaagactgggagtgaggaaga 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84339  acacagccatggtgtctcctgtcctccaccttcactggtgaagactgggagtgaggaaga 84280


Query: 312    agagtgagattgcaccctctctgcaggaccatgggcagaccctgccccttacctcttctc 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84279  agagtgagattgcaccctctctgcaggaccatgggcagaccctgccccttacctcttctc 84220


Query: 372    aggggtctctcttctctcctattaacttctttccatt 408
              ||||||||||||||||||||||| |||||||||| |||||
Sbjct: 84219  aggggtctctcttctctcctgttaacttcttcccatt 84183
```

Query= SEQ ID NO:16 (PE029)
       (403 letters)

```
                                                              Score      E
Sequences producing significant alignments:                  (bits)   Value

AP003031.3.1.95585                                             456     e-126
```

>AP003031.3.1.95585
        Length = 95585

 Score = 456 bits (230), Expect = e-126
 Identities = 240/243 (98%), Gaps = 1/243 (0%)
 Strand = Plus / Minus


```
Query: 161   gagccaagaagtcctcaaagcccttcctaaaggatggaggaacacatgaatatatacatc 220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 27019 gagccaagaagtcctcaaagcccttcctaaaggatggaggaacacatgaatatatacatc 26960


Query: 221   aaatcctccttccacagagactcactgaagggaatgaagaagggaaaagtcctcctaatt 280
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct: 26959 aaatcctccttccacagagactcactgaagggaatgaagaaggaaaaagtcctcctaatt 26900


Query: 281   attaagatgcgttccttgggactcggagaattaggaaggaaaccccaagtcttgaatac 340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 26899 attaagatgcgttccttgggactcggagaattaggaaggaaaccccaagtcttgaatac 26840


Query: 341   atttctctaaagaggccgaatacttaataatcaggggagattaaagcaaatgggagac-c 399
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Sbjct: 26839 atttctctaaagaggccgaatacttaataatcaggggagattaaagcaaatggtagacac 26780


Query: 400   cct 402
             |||
Sbjct: 26779 cct 26777
```


 Score = 311 bits (157), Expect = 2e-82
 Identities = 160/161 (99%)
 Strand = Plus / Minus


```
Query: 1     gagtctactgacagaagccaaaggttgctgctagtttcagcttcctggtgttcctcatta 60
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 37882 gagtctactgacaaaagccaaaggttgctgctagtttcagcttcctggtgttcctcatta 37823


Query: 61    ttttcaaaaatgtctgactgcatcttttggacattataaaaaccacagtaggaaaaaacg 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 37822 ttttcaaaaatgtctgactgcatcttttggacattataaaaaccacagtaggaaaaaacg 37763
```

```
Query: 121    ccagctatttcaatggaccaacaaagtgagactccaaagtg 161
              |||||||||||||||||||||||||||||||||||||||||
Sbjct: 37762 ccagctatttcaatggaccaacaaagtgagactccaaagtg 37722
```

Query= SEQ ID NO:17 (PE029)
          (445 letters)

	Score	E
Sequences producing significant alignments:	(bits)	Value

AL158141.14.1.184181   535   e-150

>AL158141.14.1.184181
        Length = 184181

 Score = 535 bits (270), Expect = e-150
 Identities = 312/329 (94%), Gaps = 2/329 (0%)
 Strand = Plus / Plus

Query: 118   agggtcttgctctgtcgcccaggctagagtgcagtggcgcaatcttggctcatggcaacc 177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9434 agggtcttgctctgtcgcccaggctagagtgcagtggcgcaatcttggctcatggcaacc 9493

Query: 178   tccacctcccgggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9494 tccacctcccgggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 9553

Query: 238   gtgcctaccaccaggcccagctaaattttttgtattttttagtacagacggggtttcgcc 297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9554 gtgcctaccaccaggcccagctaaattttttgtattttttagtacagacggggtttcgcc 9613

Query: 298   accttggccaggctggtcttgaactcctgaccttgtgatctacccacctnagnntcccaa 357
             ||||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Sbjct: 9614 accttggccaggctggtcttgaactcctgaccttgtgatctacccacctcagtctcccaa 9673

Query: 358   ngggctggnattacaggggggagagaccggacccagccaccttactgngtttctgantgn 417
             | ||||| ||||||||| | |||||||||| |||||||||||||||| ||||||||| ||
Sbjct: 9674 agtgctgggattacaggtgtgagagaccgcacccagccaccttactgagtttctgattgc 9733

Query: 418   nntttcctttcct-ttccttttcccttaa 445
               |||||| ||| |||||| ||||||||
Sbjct: 9734 tctttcctt-cctcttccttctcccttaa 9761

 Score = 238 bits (120), Expect = 2e-60
 Identities = 120/120 (100%)
 Strand = Plus / Plus

Query: 1   agacggggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatgaccctc 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8124 agacggggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatgaccctc 8183

```
Query: 61    ctgcctcagcctcccaaagtgctgcgattaaaggcacaagccactgtgcccaaccaaagg 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8184  ctgcctcagcctcccaaagtgctgcgattaaaggcacaagccactgtgcccaaccaaagg 8243
```

Query= SEQ ID NO:18 (PE029)
         (486 letters)

```
                                                                    Score       E
Sequences producing significant alignments:                        (bits)    Value

AL158141.14.1.184181                                                 599    e-169
```

>AL158141.14.1.184181
         Length = 184181

 Score = 599 bits (302), Expect = e-169
 Identities = 347/362 (95%), Gaps = 3/362 (0%)
 Strand = Plus / Plus


```
Query: 118   agggtcttgctctgtcgcccaggctagagtgcagtggcgcaatcttggctcatggcaacc 177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9434  agggtcttgctctgtcgcccaggctagagtgcagtggcgcaatcttggctcatggcaacc 9493


Query: 178   tccacctcccgggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 9494  tccacctcccgggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 9553


Query: 238   gtgcctaccaccaggcccagct-aattttttgtatttttagtacagacggggtttcgcc 296
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct: 9554  gtgcctaccaccaggcccagctaaattttttgtatttttagtacagacggggtttcgcc 9613


Query: 297   accttggccaggctggtcttgaactcctgaccttgtgatctacccacctcagtctcccaa 356
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 357   agtgctgggattacaggtgtgagagaccgcacccaggcaccttactgaggttctgaatgn 416
             ||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||| ||
Sbjct: 9674  agtgctgggattacaggtgtgagagaccgcacccagccaccttactgagtttctgattgc 9733


Query: 417   tcttttcnttctttttcctttttcccttaaattggcccaaagtttnatccttggcttttt 476
             ||||| | ||| | ||||||| | |||||||| ||| |||||||||| ||||||| ||||||
Sbjct: 9734  tctttcc-ttcctcttccttct-cccttaacttgccccaaagttttatccttgacttttt 9791


Query: 477   tt 478
             ||
Sbjct: 9792  tt 9793
```

```
Score =  238 bits (120), Expect = 3e-60
 Identities = 120/120 (100%)
 Strand = Plus / Plus


Query: 1      agacgggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatgaccctc 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8124   agacgggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatgaccctc 8183


Query: 61     ctgcctcagcctcccaaagtgctgcgattaaaggcacaagccactgtgcccaaccaaagg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8184   ctgcctcagcctcccaaagtgctgcgattaaaggcacaagccactgtgcccaaccaaagg 8243
```